

# SEQUENCE LISTING

<110> KATZ, RUTH  
JIANG, FENG

<120> DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS

<130> UTSC:658US

<140> UNKNOWN

<141> 2001-08-06

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18)..(680)

<400> 1

```

cgcctaacgc tgccaac atg gtg ttc agg cgc ttc gtg gag gtt ggc cgg      50
      Met Val Phe Arg Arg Phe Val Glu Val Gly Arg
              1              5              10

gtg gcc tat gtc tcc ttt gga cct cat gcc gga aaa ttg gtc gcg att      98
Val Ala Tyr Val Ser Phe Gly Pro His Ala Gly Lys Leu Val Ala Ile
              15              20              25

gta gat gtt att gat cag aac agg gct ttg gtc gat gga cct tgc act      146
Val Asp Val Ile Asp Gln Asn Arg Ala Leu Val Asp Gly Pro Cys Thr
              30              35              40

caa gtg agg aga cag gcc atg cct ttc aag tgc atg cag ctc act gat      194
Gln Val Arg Arg Gln Ala Met Pro Phe Lys Cys Met Gln Leu Thr Asp
              45              50              55

ttc atc ctc aag ttt ctg cac agt gcc cac cag aag tat gtc cga caa      242
Phe Ile Leu Lys Phe Leu His Ser Ala His Gln Lys Tyr Val Arg Gln
              60              65              70              75

gcc tgg cag aag gca gac atc aat aca aaa tgg gca gcc aca cga tgg      290
Ala Trp Gln Lys Ala Asp Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp
              80              85              90

gcc aag aag att gaa gcc aga gaa agg aaa gcc aag atg aca gat ttt      338
Ala Lys Lys Ile Glu Ala Arg Glu Arg Lys Ala Lys Met Thr Asp Phe
              95              100              105

gat cgt ttt aaa gtt atg aag gca aag aaa atg agg aac aga ata atc      386

```

Asp Arg Phe Lys Val Met Lys Ala Lys Lys Met Arg Asn Arg Ile Ile  
110 115 120

aag aat gaa gtt aag aag ctt caa aag gca gct ctc ctg aaa gct tct 434  
Lys Asn Glu Val Lys Lys Leu Gln Lys Ala Ala Leu Leu Lys Ala Ser  
125 130 135

ccc aaa aaa gca cct ggt act aag ggt act gct gct gct gct gct gct 482  
Pro Lys Lys Ala Pro Gly Thr Lys Gly Thr Ala Ala Ala Ala Ala Ala  
140 145 150 155

gct gct gct gct gct gct gct gct gct aaa gtt cca gca aaa aag atc 530  
Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Val Pro Ala Lys Lys Ile  
160 165 170

acc gcc gcg agt aaa aag gct cca gcc cag aag gtt cct gcc cag aaa 578  
Thr Ala Ala Ser Lys Lys Ala Pro Ala Gln Lys Val Pro Ala Gln Lys  
175 180 185

gcc aca ggc cag aaa gca gcg cct gct cca aaa gct cag aag ggt caa 626  
Ala Thr Gly Gln Lys Ala Ala Pro Ala Pro Lys Ala Gln Lys Gly Gln  
190 195 200

aaa gct cca gcc cag aaa gca cct gct cca aag gca tct ggc aag aaa 674  
Lys Ala Pro Ala Gln Lys Ala Pro Ala Pro Lys Ala Ser Gly Lys Lys  
205 210 215

gca taa gtggcaatca taaaaagtaa taaagggttct ttttgacctg tt 722  
Ala  
220

<210> 2  
<211> 220  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Val Phe Arg Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser  
1 5 10 15  
Phe Gly Pro His Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp  
20 25 30  
Gln Asn Arg Ala Leu Val Asp Gly Pro Cys Thr Gln Val Arg Arg Gln  
35 40 45  
Ala Met Pro Phe Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe  
50 55 60  
Leu His Ser Ala His Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala  
65 70 75 80  
Asp Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp Ala Lys Lys Ile Glu  
85 90 95  
Ala Arg Glu Arg Lys Ala Lys Met Thr Asp Phe Asp Arg Phe Lys Val  
100 105 110  
Met Lys Ala Lys Lys Met Arg Asn Arg Ile Ile Lys Asn Glu Val Lys  
115 120 125  
Lys Leu Gln Lys Ala Ala Leu Leu Lys Ala Ser Pro Lys Lys Ala Pro



Gln	Asp	Val	Pro	Arg	Ala	Phe	Glu	Glu	Cys	Met	Gln	Lys	Val	Lys	Gly		
			110					115					120				
cag	gtt	cca	tcc	cac	ctc	cac	gga	tcc	acc	ccc	att	cac	ctg	gga	gcc	496	
Gln	Val	Pro	Ser	His	Leu	His	Gly	Ser	Thr	Pro	Ile	His	Leu	Gly	Ala		
		125					130				135						
acg	gct	ggg	atg	cgc	ttg	ctg	agg	ttg	caa	aat	gaa	aca	gca	gct	aat	544	
Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Leu	Gln	Asn	Glu	Thr	Ala	Ala	Asn		
	140					145				150							
gaa	gtc	ctt	gaa	agc	atc	caa	agc	tac	ttc	aag	tcc	cag	ccc	ttt	gac	592	
Glu	Val	Leu	Glu	Ser	Ile	Gln	Ser	Tyr	Phe	Lys	Ser	Gln	Pro	Phe	Asp		
155					160				165						170		
ttt	agg	ggt	gct	caa	atc	att	tct	ggg	caa	gaa	gaa	ggg	gta	tat	gga	640	
Phe	Arg	Gly	Ala	Gln	Ile	Ile	Ser	Gly	Gln	Glu	Glu	Gly	Val	Tyr	Gly		
				175				180						185			
tgg	att	aca	gcc	aac	tat	tta	atg	gga	aat	ttc	ctg	gag	aag	aac	ctg	688	
Trp	Ile	Thr	Ala	Asn	Tyr	Leu	Met	Gly	Asn	Phe	Leu	Glu	Lys	Asn	Leu		
			190					195					200				
tgg	cac	atg	tgg	gtg	cac	ccg	cat	gga	gtg	gaa	acc	acg	ggt	gcc	ctg	736	
Trp	His	Met	Trp	Val	His	Pro	His	Gly	Val	Glu	Thr	Thr	Gly	Ala	Leu		
		205					210					215					
gac	tta	ggt	ggt	gcc	tcc	acc	caa	ata	tcc	ttc	gtg	gca	gga	gag	aag	784	
Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Ser	Phe	Val	Ala	Gly	Glu	Lys		
	220					225				230							
atg	gat	ctg	aac	acc	agc	gac	atc	atg	cag	gtg	tcc	ctg	tat	ggc	tac	832	
Met	Asp	Leu	Asn	Thr	Ser	Asp	Ile	Met	Gln	Val	Ser	Leu	Tyr	Gly	Tyr		
	235				240				245					250			
gta	tac	acg	ctc	tac	aca	cac	agc	ttc	cag	tgc	tat	ggc	cgg	aat	gag	880	
Val	Tyr	Thr	Leu	Tyr	Thr	His	Ser	Phe	Gln	Cys	Tyr	Gly	Arg	Asn	Glu		
				255				260						265			
gct	gag	aag	aag	ttt	ctg	gca	atg	ctc	ctg	cag	aat	tct	cct	acc	aaa	928	
Ala	Glu	Lys	Lys	Phe	Leu	Ala	Met	Leu	Leu	Gln	Asn	Ser	Pro	Thr	Lys		
			270					275				280					
aac	cat	ctc	acc	aat	ccc	tgt	tac	cct	cgg	gat	tat	agc	atc	agc	ttc	976	
Asn	His	Leu	Thr	Asn	Pro	Cys	Tyr	Pro	Arg	Asp	Tyr	Ser	Ile	Ser	Phe		
		285					290					295					
acc	atg	ggc	cat	gta	ttt	gat	agc	ctg	tgc	act	gtg	gac	cag	agg	cca	1024	
Thr	Met	Gly	His	Val	Phe	Asp	Ser	Leu	Cys	Thr	Val	Asp	Gln	Arg	Pro		
		300				305					310						
gaa	agt	tat	aac	ccc	aat	gat	gtc	atc	act	ttt	gaa	gga	act	ggg	gac	1072	
Glu	Ser	Tyr	Asn	Pro	Asn	Asp	Val	Ile	Thr	Phe	Glu	Gly	Thr	Gly	Asp		
	315				320					325					330		

cca tct ctg tgt aag gag aag gtg gct tcc ata ttt gac ttc aaa gct	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
tgc cat gat caa gaa acc tgt tct ttt gat ggg gtt tat cag cca aag	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	
att aaa ggg cca ttt gtg gct ttt gca gga ttc tac tac aca gcc agt	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	
365 370 375	
gct tta aat ctt tca ggt agc ttt tcc ctg gac acc ttc aac tcc agc	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser	
380 385 390	
acc tgg aat ttc tgc tca cag aat tgg agt cag ctc cca ctg ctg ctc	1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu	
395 400 405 410	
ccc aaa ttt gat gag gta tat gcc cgc tct tac tgc ttc tca gcc aac	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn	
415 420 425	
tac atc tac cac ttg ttt gtg aac ggt tac aaa ttc aca gag gag act	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr	
430 435 440	
tgg ccc caa ata cac ttt gaa aaa gaa gtg ggg aat agc agc ata gcc	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala	
445 450 455	
tgg tct ctt ggc tac atg ctc agc ctg acc aac cag atc cca gct gaa	1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	
460 465 470	
agc cct ctg atc cgt ctg ccc ata gaa cca cct gtc ttt gtg ggc acc	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	
475 480 485 490	
ctc gct ttc ttc aca gtg gca gcc ttg ctg tgt ctg gca ttt ctt gca	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
tac ctg tgt tca gca acc aga aga aag agg cac tcc gag cat gcc ttt	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
gac cat gca gtg gat tct gac tga gccttcaaag cagctcctgg agtccaatgg	1702
Asp His Ala Val Asp Ser Asp	
525 530	
ctgcttagag tcagcctggg tggcaccagg caatgcaggt gaagtggctg ccttcaggaa	1762
atacaactaa ctaaaatcaa acacctaggt cacgtgcctc tcaaatactg atttctgcc	1822

cagcacctct tgaggcatcc cttggctatt ctgtgcatat tggtcttcag agacctcact 1882  
 acccacatgc tgatctattg gggaacagag aagagacagg ccaactaagg caggctcttt 1942  
 atattaagtt cccagagga agagtaagtt gagaaggtat cagtttaatg ttgaagaatt 2002  
 gacctcaggg ctcagtttcc atttccctcc ctcagtattc ttcctggcaa gatacccatt 2062  
 aagcatttcg ccaatcagaa tctcatttta tagtttttcc cattgggtctt taactaagac 2122  
 tttcttgtag caatctcgta agcagtgaac cccctcagat cagtagaata tagtatctgg 2182  
 gggagaagac ttacttcctt cagggcagca gccacagcca ggcttctgtc atacaggtag 2242  
 atcccgaagc acagagacat aaaaaaggtc tcccagaaaa ctatagacca ttctccaagt 2302  
 ggaattccca cttagggctc tggtcactag attgcaacct gtgtgtttgt catcatcctc 2362  
 atctcaccat tgtattgcta tgccctccca taaaaacaca ttgatcccta gcaagattat 2422  
 tgcattccag attttactgc ctttgctagg cttttgctta gcaaagggct gactttccat 2482  
 tgttatcatg gtgtatatat ttttgcacc attcccacaa gtataactga tgttgtcata 2542  
 gaacgaacat cctactctat gatttactaa ccaattactt tcccagatca tagacctctc 2602  
 tgcatagtag tcataggtct tgactttggg gaaagaaaag gaagctgcag gaatatttat 2662  
 ctccaaagtc gaatgagaaa gaactccagc aaatccaatg gctacaaact aaaaatcagc 2722  
 attatttcat attgctgttt cttagctgaa tatggaataa agaactatta ttttattttg 2782  
 aaaaaaaaaa aaaaaa 2797

<210> 4  
 <211> 529  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Phe Thr Val Leu Thr Arg Gln Pro Cys Glu Gln Ala Gly Leu Lys  
 1 5 10 15  
 Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala Leu Val Val Leu Leu Val  
 20 25 30  
 Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln  
 35 40 45  
 Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly  
 50 55 60  
 Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu  
 65 70 75 80  
 Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly  
 85 90 95  
 Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala

				100						105					110	
Phe	Glu	Glu	Cys	Met	Gln	Lys	Val	Lys	Gly	Gln	Val	Pro	Ser	His	Leu	
		115					120				125					
His	Gly	Ser	Thr	Pro	Ile	His	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	
	130					135					140					
Leu	Arg	Leu	Gln	Asn	Glu	Thr	Ala	Ala	Asn	Glu	Val	Leu	Glu	Ser	Ile	
145					150					155					160	
Gln	Ser	Tyr	Phe	Lys	Ser	Gln	Pro	Phe	Asp	Phe	Arg	Gly	Ala	Gln	Ile	
				165					170					175		
Ile	Ser	Gly	Gln	Glu	Glu	Gly	Val	Tyr	Gly	Trp	Ile	Thr	Ala	Asn	Tyr	
			180					185					190			
Leu	Met	Gly	Asn	Phe	Leu	Glu	Lys	Asn	Leu	Trp	His	Met	Trp	Val	His	
		195					200					205				
Pro	His	Gly	Val	Glu	Thr	Thr	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	
	210					215					220					
Thr	Gln	Ile	Ser	Phe	Val	Ala	Gly	Glu	Lys	Met	Asp	Leu	Asn	Thr	Ser	
225					230					235					240	
Asp	Ile	Met	Gln	Val	Ser	Leu	Tyr	Gly	Tyr	Val	Tyr	Thr	Leu	Tyr	Thr	
				245					250					255		
His	Ser	Phe	Gln	Cys	Tyr	Gly	Arg	Asn	Glu	Ala	Glu	Lys	Lys	Phe	Leu	
			260					265					270			
Ala	Met	Leu	Leu	Gln	Asn	Ser	Pro	Thr	Lys	Asn	His	Leu	Thr	Asn	Pro	
		275					280					285				
Cys	Tyr	Pro	Arg	Asp	Tyr	Ser	Ile	Ser	Phe	Thr	Met	Gly	His	Val	Phe	
	290					295					300					
Asp	Ser	Leu	Cys	Thr	Val	Asp	Gln	Arg	Pro	Glu	Ser	Tyr	Asn	Pro	Asn	
305					310					315					320	
Asp	Val	Ile	Thr	Phe	Glu	Gly	Thr	Gly	Asp	Pro	Ser	Leu	Cys	Lys	Glu	
				325					330					335		
Lys	Val	Ala	Ser	Ile	Phe	Asp	Phe	Lys	Ala	Cys	His	Asp	Gln	Glu	Thr	
			340					345					350			
Cys	Ser	Phe	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Ile	Lys	Gly	Pro	Phe	Val	
		355					360					365				
Ala	Phe	Ala	Gly	Phe	Tyr	Tyr	Thr	Ala	Ser	Ala	Leu	Asn	Leu	Ser	Gly	
	370					375					380					
Ser	Phe	Ser	Leu	Asp	Thr	Phe	Asn	Ser	Ser	Thr	Trp	Asn	Phe	Cys	Ser	
385					390					395					400	
Gln	Asn	Trp	Ser	Gln	Leu	Pro	Leu	Leu	Leu	Pro	Lys	Phe	Asp	Glu	Val	
				405					410					415		
Tyr	Ala	Arg	Ser	Tyr	Cys	Phe	Ser	Ala	Asn	Tyr	Ile	Tyr	His	Leu	Phe	
			420					425					430			
Val	Asn	Gly	Tyr	Lys	Phe	Thr	Glu	Thr	Trp	Pro	Gln	Ile	His	Phe		
		435					440									

<210> 5  
 <211> 3771  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> prim\_transcript  
 <222> (921)..(3751)

<400> 5  
 ccatggcccc ttcattaggg ccccaattgt gactttattg ctcatagtct cttccctgcc 60  
 ttggtggctc tcatccccc aacctgaatg cagaagtctt ggtcctagac tcaactccgt 120  
 gccacccttc agcctacgtt gtgggttctt gctaagtga gcatttacct aacaatcaag 180  
 acttctgaca gtcctcagtc ctgcccccaa accccttgg atttctcttt ttcaagggtg 240  
 tttcggctag gagagtgagc gtggcttggg tgagggcaga taggggtggga gcatggggca 300  
 tgtatggatg agaccttgac aaagggaacc cggaggaaag acagggggccc tttccctctt 360  
 tgtcctggaa acccggtcga gcccagccc ttgcccattc tgctgctgct gcctgggtacc 420  
 ttcacaagg ccagactcct ctccacaaag ctgtggtctg caccagctcc tctggctctc 480  
 ctctctgccc tgctgagggc cgcctcctag cctggctgcc aatcacagga gaaaggggtt 540  
 gggattttgt ttgtgctct gtctgagcag agaatggctg ataggcactg agcgttgccc 600  
 tggagagccc ctctgtccct gctatcccca tctccctgg ccagacttc tgcccttcac 660  
 gcccatccct gaccagcagc cccactcagt ctgggctctg ggtgccagct gtatagacat 720  
 gccacctgaa ccagggccag agctgggtgat gcgtggggct attttaagca cagcctcttg 780  
 gcctgcacac tcccctggcc ccagccccc agcagctcag ctactggtca cctgccaccg 840  
 cctggaatgc tgattggcag ttggtggggg tgggtggggg ctgggaagac actattataa 900  
 agctgggagt gttgggaagc agcgtcccc gtccagagtc ctctgtggtc cctgctgcca 960  
 ccatggccac tcaccgcctc gtgatggctc ggcacggcga gagcacatgg aaccaggaga 1020  
 accgtttctg tggctgggtc gatgcagagc tgagtgaana ggggaccgag gaggccaagc 1080  
 ggggagccaa ggccatcaag gatgccaaga tggagtgtga catctgctac acgtcagtgc 1140  
 tgaagcgggc catcccgacc ctctgggcca tctggacgg cacggaccag atgtggctgc 1200  
 ctgtggtgct cacttgccgc ttcaatgagc ggcattacgg gggcctcaca ggcctcaaca 1260  
 aggcagaaac ggccgccaag cacggggagg agcagggtga gatctggagg cgctccttcg 1320  
 acatcccgcc gccccgatg gacgagaagc acccctacta caactccatt agcaagggtg 1380  
 gctgcctttg ctgggaaggc ctctgggaag ctgcagagtg gggagtcggg tgggggcccc 1440  
 ctggcttggg agggaaagca gcgtgcctgt gtcccccagg agcgtcggtg cgcaggcctg 1500  
 aagcccgggg aactcccac ctgcgagagc ctcaaggaca ccattgcccg ggccctgccc 1560  
 ttctggaacg aggagattgt tcccagatc aaggccggca agcagtgct cattgcagcc 1620  
 cacgggaaca gcctgcgggg cattgtcaag cacctggaag gtaggccacc ttcaggagcc 1680  
 tgggcagggt ggggtggcag cagccagctg gcttctcatc tcagcaaagt ctctcgccat 1740  
 gaccagcttt ctacgctggc tccacatcat tcaactgaaa gaggtgaga agccattttt 1800  
 tagttttgtg aaattttccc catttctgtg taactggaca cactccacag gggctgactg 1860  
 cactcgaagc tcgctgtgtc ccgaggtggg gcaggctcca aagggtggcat ctgccaaggg 1920  
 acaccagct aggaaacgga agggctgggc ttagagcatc tggctccaaa tcccaactta 1980  
 ctgtggggcc ctggacaagc cacctccatc tctgggcctc tcccttttcc ggggtgggtg 2040  
 ggagctcccc ctggtactga attcctcttg atgtaggctt ggacccctcg cagggcctc 2100  
 ccccatcagg tctcagaat ccctgcatga gcttcaccac ctatctccct ctggagcccc 2160  
 tctctgggca aaggaaaagc caatcaaaag aggggtgcag gactatggag tggccagact 2220  
 ctgggcttgc agctgggctc ccactgaaga gcaagggtg acaaatgggc ccgggatgca 2280  
 tgggcgcagt aaggcctcgc ccagagtgc tggcacctcc gtccgcctcc caccttagta 2340  
 ttctgacaca agggcagtc aaattagcat ctgaatgacc ttaaagcttg ttgagtcctg 2400  
 gaaaggctag aagggtgtgc ccagacctc ctgctcctag ggccgttggg cagttggcca 2460  
 gagcaccag accggcaggc cccggagacc cagccagccc caagcctgcc cgtccaaac 2520  
 acggacacct ggcacctggc actggggcca ggcagagggg aggaccacct gctcctctc 2580



```

ccttccggag acttcatgca gccccatgac cctcccacag cctggtttgg ggaaagggga 2640
cgcacttttg gtggtgaata tgagggattt cactctgact ccccagagaa cattttctta 2700
aaccctccc tgcacggagc aggggtggag tggcgcaaac atcaaaggct gagctgctat 2760
tcccagctca ggggctgcag gaggcaggca gggtcagggt tcgaccaggc tcggcctccc 2820
tgtccctcct ccagctccat tccgcacttg ctccctctgtt caggatgtct agaatttaga 2880
gcactttaga aacaaaggtt gctgggcacg gtggtcact cctgtaatcc cagcactttg 2940
ggaggtgag gcaggcagat cacctgaggt caggagtttg agaccagcct gaccaacatg 3000
gtaaaacccg tttctactaa aaatacaaaa ttagccgggt gtggtggcgc tcacctgtaa 3060
tcccagctac ttgggaggct gaggcagaat cacttcaacc caggagatgg aggttgagcgt 3120
gagccaagat cgtgccactg cactccagcc tgggcaagag gagtaaaact ccactctcaa 3180
aaaaagaaaa agaaaaagaa aagaaaaaaa aaaaccaaag ggtgagtgtc ccttccctgac 3240
cctcaacttc agtctggctg gattcacact gggctgaggg aactatggac agcaccacca 3300
cagatcacag ccacttgggt ggggctgaag tccccatttt ttccaccact gggctatttc 3360
tgtaggctgc ttggtctaac tcagttactc cttgaccttt ggcaacattt ctgtggcctc 3420
gttctcaggg ctgggaagga attggtgcca ggggaactgg ctctgtggac cataaaggctc 3480
acatagtgtc tgctgtgtaa acaggctggg gacagagggg ctaaggacac ctattccttc 3540
cggcataggg atgtcagacc aggcgatcat ggagctgaac ctgcccacgg ggatcccat 3600
tgtgtatgag ctgaacaagg agctgaagcc caccaagccc atgcagttcc tgggtgatga 3660
ggaaacggtg cggaaggcca tggaggctgt ggctgccag ggcaaggcca agtgaggggt 3720
gggcttgggc aataaaggca cctcccccaa cagcctggag tctccagcgc a 3771

```

<210> 6  
 <211> 992  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (242) .. (583)

<400> 6  
 ttttgtgcga gagccgcagc gccgcctctt ctctcgcgcc ctgcctctt cctccgcctc 60  
  
 ctccctcgcc tcttccctgcc tcctcccggc ttccgcccgc gccactccag cctaattcca 120  
  
 accccagggc gaaggttttc ttattttattt ccgtttttctc gccactacag cctcctgaca 180  
  
 aggtgatccg ggcgggcccc gcaggaattt tatccctca ccggcctcac actagtatcg 240  
  
 c atg tcc act atc cag aac ctc caa tct ttc gac ccc ttt gct gat gca 289  
 Met Ser Thr Ile Gln Asn Leu Gln Ser Phe Asp Pro Phe Ala Asp Ala  
 1 5 10 15  
  
 act aag ggt gac gac tta ctc ccg gca ggg act gag gat tac att cat 337  
 Thr Lys Gly Asp Asp Leu Leu Pro Ala Gly Thr Glu Asp Tyr Ile His  
 20 25 30  
  
 ata aga atc cag caa cgg aac ggc aga aag aca ctg act act gtt cag 385  
 Ile Arg Ile Gln Gln Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln  
 35 40 45  
  
 ggc att gca gat gat tat gac aaa aag aaa ctt gtg aaa gct ttc aaa 433  
 Gly Ile Ala Asp Asp Tyr Asp Lys Lys Lys Leu Val Lys Ala Phe Lys  
 50 55 60

aag aaa ttt gcc tgt aat ggt act gtg att gaa cat cct gaa tac gga 481  
 Lys Lys Phe Ala Cys Asn Gly Thr Val Ile Glu His Pro Glu Tyr Gly  
 65 70 75 80

gag gtt att cag ctt caa ggt gac caa aga aaa aac atc tgc cag ttt 529  
 Glu Val Ile Gln Leu Gln Gly Asp Gln Arg Lys Asn Ile Cys Gln Phe  
 85 90 95

ctc ttg gag gtt ggc att gta aag gag gaa cag ctt aag gtt cat gga 577  
 Leu Leu Glu Val Gly Ile Val Lys Glu Glu Gln Leu Lys Val His Gly  
 100 105 110

ttc taa aatgaacct aatacgtgga gaatttcttg aatagttttg ttctctaaac 633  
 Phe

ccggtttggc tgccttgatga aatgattccc tgcagtaaac ggacttttca tttatttaac 693

cattcaaact tccattcaca tctgcatgat tacagaaaac atgggggtatg tagactagta 753

acacataaga aaattgcagt aagatggtaa caaacctca tattgtcttt acatgtttcc 813

aatggaaaat gttttgagtg tttattgttc agtttattac gtttcacttg attaaatttt 873

ttttgttggt gtattaaacc atgtacgttg cagcttaaca ataaaaaaaa aatctatgaa 933

tctttgtgag caattatgct cccaaatcta agcaagtaat aaagaagggg gattcaaag 992

<210> 7

<211> 113

<212> PRT

<213> Homo sapiens

<400> 7

Met Ser Thr Ile Gln Asn Leu Gln Ser Phe Asp Pro Phe Ala Asp Ala  
 1 5 10 15  
 Thr Lys Gly Asp Asp Leu Leu Pro Ala Gly Thr Glu Asp Tyr Ile His  
 20 25 30  
 Ile Arg Ile Gln Gln Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln  
 35 40 45  
 Gly Ile Ala Asp Asp Tyr Asp Lys Lys Lys Leu Val Lys Ala Phe Lys  
 50 55 60  
 Lys Lys Phe Ala Cys Asn Gly Thr Val Ile Glu His Pro Glu Tyr Gly  
 65 70 75 80  
 Glu Val Ile Gln Leu Gln Gly Asp Gln Arg Lys Asn Ile Cys Gln Phe  
 85 90 95  
 Leu Leu Glu Val Gly Ile Val Lys Glu Glu Gln Leu Lys Val His Gly  
 100 105 110  
 Phe

<210> 8

<211> 445

<212> DNA  
<213> Homo sapiens

<400> 8  
caccatgtcc actatccaga acctccaatc tttcgacccc tttgctgatg caactaaggg 60  
tgacgactta ctcccggcag ggactgagga ttacattcat ataagaatcc agcaacggaa 120  
cggcagaaaag aactgacta ctgttcaggg cattgcagat gattatgaca aaaagaaact 180  
tgtgaaagct ttcaaaaaga aatttgctg taatgggtact gtgattgaac atcctgaata 240  
cggagaggtt attcagcttc aaggtgacca aagaaaaaac atctgccagt ttctcttgga 300  
ggttggcatt gtaaaggagg aacagcttaa ggttcatgga ttcaagggcg agcttcgagg 360  
tcaccattc gaaggttaagc ctatccctaa cctctcctc ggtctcgatt ctacgcgtac 420  
cggtcacat caccatcacc attga 445

<210> 9  
<211> 146  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 9  
Met Ser Thr Ile Gln Asn Leu Gln Ser Phe Asp Pro Phe Ala Asp Ala  
1 5 10 15  
Thr Lys Gly Asp Asp Leu Leu Pro Ala Gly Thr Glu Asp Tyr Ile His  
20 25 30  
Ile Arg Ile Gln Gln Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln  
35 40 45  
Gly Ile Ala Asp Asp Tyr Asp Lys Lys Lys Leu Val Lys Ala Phe Lys  
50 55 60  
Lys Lys Phe Ala Cys Asn Gly Thr Val Ile Glu His Pro Glu Tyr Gly  
65 70 75 80  
Glu Val Ile Gln Leu Gln Gly Asp Gln Arg Lys Asn Ile Cys Gln Phe  
85 90 95  
Leu Leu Glu Val Gly Ile Val Lys Glu Glu Gln Leu Lys Val His Gly  
100 105 110  
Phe Lys Gly Glu Leu Arg Gly His Pro Phe Glu Gly Lys Pro Ile Pro  
115 120 125  
Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His  
130 135 140  
His His  
145

<210> 10  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 10  
caccatgtcc actatccaga acctcc

26

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 11  
gaatccatga accttaagct gttc

24